Bacterial tenants in fungal quarters

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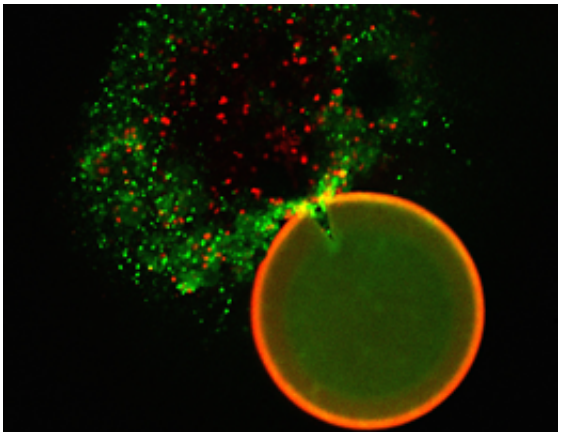

A spore produced by the mycorrhizal fungus Claroideoglomus claroideum releases endobacteria (green) and fungal cell nuclei (red). Credit: Maria Naumann, Turin University

Ludwig Maximilian University of Munich researchers have sequenced the genome of a bacterial symbiont hosted by a mycorrhizal fungus. Analysis of the symbiont's genetic endowment reveals previously unknown facets of the partnership between this odd couple.

More than 80% of all land plants harbor so-called arbuscular mycorrhizal fungi in their roots. These fungi take up inorganic nutrients from the soil and make them available to the host plant. In return, the plant supplies the fungi with carbohydrates. It is now clear that this type of symbiotic partnership, which is essential for the survival of many plant species, evolved more than 400 million years ago. "But the

mycorrhizal fungi themselves shelter symbionts of their own – endobacterial symbionts, about which very little is known," says Dr. Gloria Torres-Cortés, a member of Dr. Arthur Schüßler's research group, which is devoted to elucidating "arbuscular mycorrhiza and Geosiphon symbioses". Torres-Cortés has now determined the sequence of the genome of one member of the family of so-called Mollicutes-related endobacteria (MRE). The analysis affords new insights into the evolution of this group of prokaryotes that are found as symbionts in many species of mycorrhizal fungi.

Members of the MRE depend on their partners for survival and have not been successfully cultured in the laboratory. "For this reason, their mode of function and their interactions with their hosts cannot be investigated directly," says Torres-Cortés. "Our analysis of the genes they carry now allows us, for the first time, to make inferences about their biological properties." The MRE species studied by Torres-Cortés and her colleagues are found in the cytoplasm of the mycorrhizal fungus Dentiscutata heterogama, and are therefore referred to as DhMRE.

Borrowed genes with a long history

The new study reveals that DhMRE belongs to a previously unknown lineage, which is closely related to the bacterial genus Mycoplasma. Although many representatives of this genus are well-known as parasites that infect humans and other animal species, DhMRE is the first mycoplasma-like form yet discovered that utilizes a fungus as its host. Not only that – DhMRE is uniquely well adapted for survival in its fungal host. The sequence of the DhMRE reveals that the cell's metabolic capacity is highly impoverished, which implies that it is dependent on its host for most of its nutrients. Moreover, there has apparently been a surprisingly high level of gene transfer between the eukaryotic fungus and the prokaryotic bacterium. Thus the DhMRE genome codes for many proteins whose functions remain unknown but

which show striking similarities to fungal proteins. These factors are very probably involved in regulating the interactions between host and bacterium required to maintain their symbiotic relationship.

The symbiosis between MRE species and mycorrhizal fungi is very probably an evolutionarily ancient phenomenon. Many of the proteins encoded by the DhMRE genome clearly resemble proteins specified by the nuclear genomes of mycorrhizal fungi that do not enter into symbiotic relationships with members of the MRE. "Our data suggest that the bacterio-fungal symbiosis had already been established by the time the ancestors of today's mycorrhizal orders diverged from each other over 400 million years ago," Torres-Cortés says. "The findings also pose new questions concerning the role of the endobacteria in the development of their fungal hosts. Our study now provides the basis for a more focused search for other factors that are involved in the development of arbuscular mycorrhiza."

More information: "Mosaic genome of endobacteria in arbuscular mycorrhizal fungi: Transkingdom gene transfer in an ancient mycoplasma-fungus association." *PNAS* 2015 ; published ahead of print May 11, 2015, DOI: 10.1073/pnas.1501540112

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